SEQUENCE LISTING

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MIYAMURA, KOICHI

<120> CELL SEPARATION DEVICE AND SEPARATION METHOD

<130> ASAHI-1-PC-1

<140> 09/701,001
<141> 2000-11-22

<150> PCT/JP99/02711
<151> 1999-05-24

<150> JP 159957
<151> 1998-05-25

<150> JP 163023
<151> 1998-05-26

<160> 66

<170> PatentIn Ver. 2.1

<210> 1
<211> 5
<212> PRT
<213> Mus sp.

see EP 0365205 Figs 2 and 3

H chain CDR1

<400> 1
Asp Tyr Val Ile Asn
1 5

= CDR1 of anti Lewis a

<210> 2
<211> 17
<212> PRT
<213> Mus sp.

H chain CDR2

<400> 2
Glu Ile Tyr Pro Gly Ser Gly Ser Ala Tyr Tyr Asn Glu Met Phe Lys
1 5 10 15

Gly

= CDR2 of anti Lewis a

<210> 3
<211> 9
<212> PRT
<213> Mus sp.

H chain CDR3

<400> 3
Arg Gly Thr Gly Thr Gly Phe Ala Tyr
1 5

= CDR3 of anti Lewis a

L chain CDR 1

<210> 4
<211> 15
<212> PRT
<213> Mus sp.

<400> 4
Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn
1 5 10 15

CDR 1 of anti-LewBa

L chain CDR 2

<210> 5
<211> 7
<212> PRT
<213> Mus sp.

<400> 5
Ala Ala Ser Asn Leu Glu Ser
1 5

CDR2 of anti-LewBa

L chain CDR 3

<210> 6
<211> 9
<212> PRT
<213> Mus sp.

<400> 6
Gln Gln Ser Ser Glu Asp Pro Pro Thr
1 5

CDR3 of anti-LewBa

<210> 7
<211> 330
<212> DNA
<213> Mus sp.

<220>
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<222> (1)..(330)

<400> 7

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cct gag ctg gtg aag cct ggg gct tca gtg aag atg tcc tgc aag gct   48
Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala
 1               5                  10                  15

tct gga tac aca ttc act gac tat gtt ata aac tgg ttg aac cag aga   96
Ser Gly Tyr Thr Phe Thr Asp Tyr Val Ile Asn Trp Leu Asn Gln Arg
            20                  25                  30

act gga cag ggc ctt gag tgg att gga gag att tat cct gga agt ggt   144
Thr Gly Gln Gly Leu Glu Trp Ile Gly Glu Ile Tyr Pro Gly Ser Gly
        35                  40                  45

agt gct tac tac aat gag atg ttc aag ggc aag gcc aca ctg act gca   192
Ser Ala Tyr Tyr Asn Glu Met Phe Lys Gly Lys Ala Thr Leu Thr Ala
    50                  55                  60
```

```
gac aaa tcc tcc aac aca gcc tac atg cag ctc agc agc ctg aca tct   240
Asp Lys Ser Ser Asn Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser
 65                  70                  75                  80

gag gac tct gcg gtc tat ttc tgt gca aga cgc gga act ggg acg ggg   288
Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Thr Gly Thr Gly
                85                  90                  95

ttt gct tac tgg ggc cga ggg act ctg gtc act gtc tct gca           330
Phe Ala Tyr Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ala
            100                 105                 110
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<210> 8
<211> 309
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(309)

<400> 8

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gct tct ttg gct gtg tct cta ggg cag agg gcc acc atc tcc tgc aag   48
Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys
  1               5                  10                  15

gcc agc caa agt gtt gat tat gat ggt gat agt tat atg aac tgg tac   96
Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr
             20                  25                  30

caa cag aaa cca gga cag cca ccc aaa ctc ctc atc tat gct gca tcc   144
Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser
         35                  40                  45

aat cta gaa tct ggg atc cca gcc agg ttt agt ggc agt ggg tct ggg   192
Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
     50                  55                  60

aca gac ttc acc ctc aac atc cat cct gtg gag gag gag gat gct gca   240
Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala
 65                  70                  75                  80

acc tat tac tgt cag caa agt agt gag gat cct ccg acg ttc ggt gga   288
Thr Tyr Tyr Cys Gln Gln Ser Ser Glu Asp Pro Pro Thr Phe Gly Gly
                85                  90                  95

ggc acc aag ctg gaa atc aaa                                      309
Gly Thr Lys Leu Glu Ile Lys
            100
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<210> 9
<211> 925
<212> DNA
<213> Mus sp.

single chain Ab to CD4

<220>
<221> CDS
<222> (1)..(915)

<400> 9

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Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
  1               5                  10                  15

gcc cag ccg gcc atg gcc gac att gtg ctg acc caa tct cca gct tct   96
Ala Gln Pro Ala Met Ala Asp Ile Val Leu Thr Gln Ser Pro Ala Ser
             20                  25                  30

ttg gct gtg tct cta ggg cag agg gcc acc atc tcc tgc aag gcc agc  144
Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser
         35                  40                  45

caa agt gtt gat tat gat ggt gat agt tat atg aac tgg tac caa cag  192
Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln
     50                  55                  60
                                  CDR 4

aaa cca gga cag cca ccc aaa ctc ctc atc tat gct gca tcc aat cta  240
Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu
 65                  70                  75                  80
                                                  CDR 5

gaa tct ggg atc cca gcc agg ttt agt ggc agt ggg tct ggg aca gac  288
Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
             85                  90                  95

ttc acc ctc aac atc cat cct gtg gag gag gag gat gct gca acc tat  336
Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr
        100                 105                 110

tac tgt cag caa agt agt gag gat cct ccg acg ttc ggt gga ggc acc  384
Tyr Cys Gln Gln Ser Ser Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr
    115                 120                 125
                              CDR 6

aag ctg gaa atc aaa ggt gga ggc ggt tca ggc gga ggt ggc tcc gga  432
Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130                 135                 140

ggt ggc gga tcg cag gtt cag ctg cag cag tct gga cct gag ctg gtg  480
Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val
145                 150                 155                 160
    linker

aag cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga tac aca  528
Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr
                165                 170                 175

ttc act gac tat gtt ata aac tgg ttg aac cag aga act gga cag ggc  576
Phe Thr Asp Tyr Val Ile Asn Trp Leu Asn Gln Arg Thr Gly Gln Gly
        180         CDR 1   185                 190

ctt gag tgg att gga gag att tat cct gga agt ggt agt gct tac tac  624
Leu Glu Trp Ile Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ala Tyr Tyr
    195                 200                 205
                                                  CDR 2
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aat gag atg ttc aag ggc aag gcc aca ctg act gca gac aaa tcc tcc 672
Asn Glu Met Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser
210 215 220

aac aca gcc tac atg cag ctc agc agc ctg aca tct gag gac tct gcg 720
Asn Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala
225 230 235 240

gtc tat ttc tgt gca aga cgc gga act ggg acg ggg ttt gct tac tgg 768
Val Tyr Phe Cys Ala Arg Arg Gly Thr Gly Thr Gly Phe Ala Tyr Trp
245 250 255

ggc cga ggg act ctg gtc act gtc tct gca gcg gcc gca gac tac aag 816
Gly Arg Gly Thr Leu Val Thr Val Ser Ala Ala Ala Ala Asp Tyr Lys
260 265 270

gat gac gat gac aaa ggc tcg agc gag cag aag ctg atc agc gaa gag 864
Asp Asp Asp Asp Lys Gly Ser Ser Glu Gln Lys Leu Ile Ser Glu Glu
275 280 285

gat ctg ggc tcg agg tcg acc cac cat cat cat cac cac ggg tcg acc 912
Asp Leu Gly Ser Arg Ser Thr His His His His His His Gly Ser Thr
290 295 300

aaa tgataagctt 925
Lys
305

<210> 10
<211> 925
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(915)

<400> 10
atg aaa tac ctg ctg ccg acc gct gct gct ggt ctg ctg ctc ctc gcg 48
Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15

gcc cag ccg gcc atg gcc cag gtt cag ctg cag cag tct gga cct gag 96
Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Gln Ser Gly Pro Glu
20 25 30

ctg gtg aag cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga 144
Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
35 40 45

tac aca ttc act gac tat gtt ata aac tgg ttg aac cag aga act gga 192
Tyr Thr Phe Thr Asp Tyr Val Ile Asn Trp Leu Asn Gln Arg Thr Gly
50 55 60

cag ggc ctt gag tgg att gga gag att tat cct gga agt ggt agt gct 240
Gln Gly Leu Glu Trp Ile Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ala
65 70 75 80

```
tac tac aat gag atg ttc aag ggc aag gcc aca ctg act gca gac aaa   288
Tyr Tyr Asn Glu Met Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys
                 85                  90                  95

tcc tcc aac aca gcc tac atg cag ctc agc agc ctg aca tct gag gac   336
Ser Ser Asn Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
            100                 105                 110

tct gcg gtc tat ttc tgt gca aga cgc gga act ggg acg ggg ttt gct   384
Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Thr Gly Thr Gly Phe Ala
        115                 120                 125

tac tgg ggc cga ggg act ctg gtc act gtc tct gca ggt gga ggc ggt   432
Tyr Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly
    130                 135                 140

tca ggc gga ggt ggc tcc gga ggt ggc gga tcg gac att gtg ctg acc   480
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu Thr
145                 150                 155                 160

caa tct cca gct tct ttg gct gtg tct cta ggg cag agg gcc acc atc   528
Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
                165                 170                 175

tcc tgc aag gcc agc caa agt gtt gat tat gat ggt gat agt tat atg   576
Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met
            180                 185                 190

aac tgg tac caa cag aaa cca gga cag cca ccc aaa ctc ctc atc tat   624
Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
        195                 200                 205

gct gca tcc aat cta gaa tct ggg atc cca gcc agg ttt agt ggc agt   672
Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
    210                 215                 220

ggg tct ggg aca gac ttc acc ctc aac atc cat cct gtg gag gag gag   720
Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu
225                 230                 235                 240

gat gct gca acc tat tac tgt cag caa agt agt gag gat cct ccg acg   768
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Ser Glu Asp Pro Pro Thr
                245                 250                 255

ttc ggt gga ggc acc aag ctg gaa atc aaa gcg gcc gca gac tac aag   816
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ala Ala Ala Asp Tyr Lys
            260                 265                 270

gat gac gat gac aaa ggc tcg agc gag cag aag ctg atc agc gaa gag   864
Asp Asp Asp Asp Lys Gly Ser Ser Glu Gln Lys Leu Ile Ser Glu Glu
        275                 280                 285

gat ctg ggc tcg agg tcg acc cac cat cat cat cac cac ggg tcg acc   912
Asp Leu Gly Ser Arg Ser Thr His His His His His His Gly Ser Thr
    290                 295                 300
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aaa tgataagctt 925
Lys
305

<210> 11
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

<400> 11
aagcttatga accggggagt ccctttta 28

<210> 12
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

<400> 12
gcggccgctc acttgtcatc gtcgtccttg tagtctggct gcaccggggt ggacca 56

<210> 13
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

<400> 13
gggaattcat graatgsasc tgggtywtyc tctt 34

<210> 14
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

<220>
<221> modified_base
<222> (30)
<223> a, t, c, g, other or unknown

<400> 14
cccaagcttc cagggrccar kggataracn grtgg 35

<210> 15
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Single strand DNA primer for PCR

<220>
<221> modified_base
<222> (15)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (18)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (27)
<223> a, t, c, g, other or unknown

<400> 15
tgtgccctcg agctnacnca ragyccngc 29

<210> 16
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Single strand DNA primer for PCR

<400> 16
atggatacta gtggtgcagc atcagccc 28

<210> 17
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Single strand DNA primer for PCR

<400> 17
gggaattcat ggagacagac acactcctgc tat 33

<210> 18
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

<400> 18
cgtcggagga tcctcactac t 21

<210> 19
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

<400> 19
caggatccgc tgcagcagtc tggacct 27

<210> 20
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

<400> 20
tgggcccgtc gttttggctg cagagac 27

<210> 21
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

<400> 21
tcatgaaata cctgctgccg accgctgctg ctggtctgct gctcctcgcg gcccag 56

<210> 22
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

<400> 22
tgcggccgca gccatggtgt ttgcggccat cgccggctgg gccgcgagga gcagca 56

<210> 23
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

<400> 23
tgcggccgca gactacaagg atgacgatga caaaggctcg agcgagcaga agctga 56

<210> 24
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

<400> 24
ggtgggtcga cctcgagccc agatcctctt cgctgatcag cttctgctcg ctcgagc 57

<210> 25
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

<400> 25
tgcggccgca gactacaagg atg 23

<210> 26
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

<400> 26
taagcttatc atttggtcga cccgtggtga tgatgatggt gggtcgacct cgagcc 56

<210> 27
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

<400> 27
agccggccat ggccgacatt gtgctgaccc aatctcca 38

<210> 28
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

<400> 28
ctccggagcc acctccgcct gaaccgcctc cacctttgat ttccagcttg gtgcctcc 58

<210> 29
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

<400> 29
ctccggaggt ggcggatcgc aggttcagct gcagcagtct 40

<210> 30
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

<400> 30
tgcggccgct gcagagacag tgaccagagt c 31

<210> 31
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

<400> 31
agccggccat ggcccaggtt cagctgcagc agtct 35

<210> 32
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

<400> 32
ctccggagcc acctccgcct gaaccgcctc cacctgcaga gacagtgacc agagtc 56

<210> 33
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

<400> 33
ctccggaggt ggcggatcgg acattgtgct gacccaatct cca 43

<210> 34
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Single strand
DNA primer for PCR

<400> 34
tgcggccgct ttgatttcca gcttggtgcc tcc 33

<210> 35
<211> 118
<212> PRT
<213> Mus sp.

<400> 35
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

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Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30

Val Ile Asn Trp Leu Asn Gln Arg Thr Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45

Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ala Tyr Tyr Asn Glu Met Phe
    50                  55                  60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Asn Thr Ala Tyr
65                  70                  75                  80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85                  90                  95

Ala Arg Arg Gly Thr Gly Thr Gly Phe Ala Tyr Trp Gly Arg Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ala
        115
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<210> 36
<211> 111
<212> PRT
<213> Mus sp.

<400> 36

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Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
  1               5                  10                  15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
            20                  25                  30

Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45

Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala
    50                  55                  60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65                  70                  75                  80

Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Ser
                85                  90                  95

Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
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<210> 37
<211> 354
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(354)

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Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

tca gtg aag atg tcc tgc aag gct tct gga tac aca ttc act gac tat 96
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

gtt ata aac tgg ttg aac cag aga act gga cag ggc ctt gag tgg att 144
Val Ile Asn Trp Leu Asn Gln Arg Thr Gly Gln Gly Leu Glu Trp Ile
35 40 45

gga gag att tat cct gga agt ggt agt gct tac tac aat gag atg ttc 192
Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ala Tyr Tyr Asn Glu Met Phe
50 55 60

aag ggc aag gcc aca ctg act gca gac aaa tcc tcc aac aca gcc tac 240
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Asn Thr Ala Tyr
65 70 75 80

atg cag ctc agc agc ctg aca tct gag gac tct gcg gtc tat ttc tgt 288
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

gca aga cgc gga act ggg acg ggg ttt gct tac tgg ggc cga ggg act 336
Ala Arg Arg Gly Thr Gly Thr Gly Phe Ala Tyr Trp Gly Arg Gly Thr
100 105 110

ctg gtc act gtc tct gca 354
Leu Val Thr Val Ser Ala
115

<210> 38
<211> 333
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(333)

<400> 38
gac att gtg ctg acc caa tct cca gct tct ttg gct gtg tct cta ggg 48
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

cag agg gcc acc atc tcc tgc aag gcc agc caa agt gtt gat tat gat 96
Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30

ggt gat agt tat atg aac tgg tac caa cag aaa cca gga cag cca ccc 144
Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

```
aaa ctc ctc atc tat gct gca tcc aat cta gaa tct ggg atc cca gcc   192
Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala
     50                  55                  60

agg ttt agt ggc agt ggg tct ggg aca gac ttc acc ctc aac atc cat   240
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65                  70                  75                  80

cct gtg gag gag gag gat gct gca acc tat tac tgt cag caa agt agt   288
Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Ser
                85                  90                  95

gag gat cct ccg acg ttc ggt gga ggc acc aag ctg gaa atc aaa       333
Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110


<210> 39
<211> 351
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(351)

<400> 39
cag gtg cag ctg aag cag tca gga cct ggc cta gtg cag ccc tca cag   48
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
  1               5                  10                  15

agc ctg tcc ttc atc tgc aca gtc tct ggt ttc tca tta act agt cat   96
Ser Leu Ser Phe Ile Cys Thr Val Ser Gly Phe Ser Leu Thr Ser His
            20                  25                  30

ggt gta cac tgg gtt cgc cag tct cca gga aag ggt ctg gag tgg ctg   144
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45

gga gtg ata tgg ggt gct gga agg aca gac tat aat gca gct ttc ata   192
Gly Val Ile Trp Gly Ala Gly Arg Thr Asp Tyr Asn Ala Ala Phe Ile
     50                  55                  60

tcc aga ctg agc atc agc agg gac att tcc aag agc caa gtt ttc ttt   240
Ser Arg Leu Ser Ile Ser Arg Asp Ile Ser Lys Ser Gln Val Phe Phe
 65                  70                  75                  80

aag atg aac agt ctg caa gtt gat gac aca gcc ata tat tac tgt gcc   288
Lys Met Asn Ser Leu Gln Val Asp Asp Thr Ala Ile Tyr Tyr Cys Ala
                85                  90                  95

aga aat agg tac gag agc tac ttt gac tac tgg ggc caa ggc acc act   336
Arg Asn Arg Tyr Glu Ser Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
            100                 105                 110

tcc ctc aca gtc tcc                                               351
Ser Leu Thr Val Ser
        115
```

<210> 40
<211> 339
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(339)

<400> 40

```
gat gtt gtg atg acc caa act cca ctc tcc ctg cct gtc agt ctt gga   48
Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
  1               5                  10                  15

gat cag gcc tcc atc tct tgc aga tct agt cag aac ctt gta cac agt   96
Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Leu Val His Ser
             20                  25                  30

aat gga aat acc tat tta cat tgg tac ctg cag aag cca ggc cag tct   144
Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
         35                  40                  45

cca aat ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca   192
Pro Asn Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
     50                  55                  60

gac agg ttc agt ggc agt gga tca ggg aca gaa ttc aca ctc aag atc   240
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Lys Ile
 65                  70                  75                  80

agc aga gtg gag gct gag gat ctg gga gtt tat ttc tgc tct caa agt   288
Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
                 85                  90                  95

aca cat gtt ccg ctc acg ttc ggt gct ggg acc aag gtg gag ctg aaa   336
Thr His Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Val Glu Leu Lys
            100                 105                 110

cgg                                                               339
Arg
```

<210> 41
<211> 909
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(906)

<400> 41

```
atg acc atg att acg cca agc ttt gga gcc ttt ttt ttg gag att ttc   48
Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile Phe
  1               5                  10                  15
```

```
aac gtg aaa aaa tta tta ttc gca att cct tta gtt gtt cct ttc tat   96
Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr
             20                  25                  30

gcg gcc cag ccg gcc atg gcc cag gtg aag ctg cag cag tct gga cct  144
Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu Gln Gln Ser Gly Pro
         35                  40                  45

ggc cta gtg cag ccc tca cag agc ctg tcc ttc atc tgc aca gtc tct  192
Gly Leu Val Gln Pro Ser Gln Ser Leu Ser Phe Ile Cys Thr Val Ser
     50                  55                  60

ggt ttc tca tta act agt cat ggt gta cac tgg gtt cgc cag tct cca  240
Gly Phe Ser Leu Thr Ser His Gly Val His Trp Val Arg Gln Ser Pro
 65                  70                  75                  80

gga aag ggt ctg gag tgg ctg gga gtg ata tgg ggt gct gga agg aca  288
Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ala Gly Arg Thr
                 85                  90                  95

gac tat aat gca gct ttc ata tcc aga ctg agc atc agc agg gac att  336
Asp Tyr Asn Ala Ala Phe Ile Ser Arg Leu Ser Ile Ser Arg Asp Ile
            100                 105                 110

tcc aag agc caa gtt ttc ttt aag atg aac agt ctg caa gtt gat gac  384
Ser Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Val Asp Asp
        115                 120                 125

aca gcc ata tat tac tgt gcc aga aat agg tac gag agc tac ttt gac  432
Thr Ala Ile Tyr Tyr Cys Ala Arg Asn Arg Tyr Glu Ser Tyr Phe Asp
    130                 135                 140

tac tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt gga ggc ggt  480
Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
145                 150                 155                 160

tca ggc gga ggt ggc tct ggc ggt ggc gga tcg gac atc gag ctc act  528
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr
                165                 170                 175

cag tct cca ctc tcc ctg cct gtc agt ctt gga gat cag gcc tcc atc  576
Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile
            180                 185                 190

tct tgc aga tct agt cag aac ctt gta cac agt aat gga aat acc tat  624
Ser Cys Arg Ser Ser Gln Asn Leu Val His Ser Asn Gly Asn Thr Tyr
        195                 200                 205

tta cat tgg tac ctg cag aag cca ggc cag tct cca aat ctc ctg atc  672
Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Asn Leu Leu Ile
    210                 215                 220

tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc  720
Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly
225                 230                 235                 240
```

```
agt gga tca ggg aca gaa ttc aca ctc aag atc agc aga gtg gag gct      768
Ser Gly Ser Gly Thr Glu Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
                245                 250                 255

gag gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg ctc      816
Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Leu
            260                 265                 270

acg ttc ggt gct ggg acc aag gtg gag ctg aaa cgg gcg gcc gca ggt      864
Thr Phe Gly Ala Gly Thr Lys Val Glu Leu Lys Arg Ala Ala Ala Gly
        275                 280                 285

gcg ccg gtg ccg tat ccg gat ccg ctg gaa ccg cgt gcc gca tag          909
Ala Pro Val Pro Tyr Pro Asp Pro Leu Glu Pro Arg Ala Ala
    290                 295                 300


<210> 42
<211> 918
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(915)

<400> 42
atg acc atg att acg cca agc ttt gga gcc ttt ttt ttg gag att ttc      48
Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile Phe
  1               5                  10                  15

aac gtg aaa aaa tta tta ttc gca att cct tta gtt gtt cct ttc tat      96
Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr
             20                  25                  30

gcg gcc cag ccg gcc atg gcc cag gtg aag ctg cag cag tct gga cct      144
Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu Gln Gln Ser Gly Pro
         35                  40                  45

ggc cta gtg cag ccc tca cag agc ctg tcc ttc atc tgc aca gtc tct      192
Gly Leu Val Gln Pro Ser Gln Ser Leu Ser Phe Ile Cys Thr Val Ser
     50                  55                  60

ggt ttc tca tta act agt cat ggt gta cac tgg gtt cgc cag tct cca      240
Gly Phe Ser Leu Thr Ser His Gly Val His Trp Val Arg Gln Ser Pro
 65                  70                  75                  80

gga aag ggt ctg gag tgg ctg gga gtg ata tgg ggt gct gga agg aca      288
Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ala Gly Arg Thr
                 85                  90                  95

gac tat aat gca gct ttc ata tcc aga ctg agc atc agc agg gac att      336
Asp Tyr Asn Ala Ala Phe Ile Ser Arg Leu Ser Ile Ser Arg Asp Ile
            100                 105                 110

tcc aag agc caa gtt ttc ttt aag atg aac agt ctg caa gtt gat gac      384
Ser Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Val Asp Asp
        115                 120                 125
```

```
aca gcc ata tat tac tgt gcc aga aat agg tac gag agc tac ttt gac   432
Thr Ala Ile Tyr Tyr Cys Ala Arg Asn Arg Tyr Glu Ser Tyr Phe Asp
    130                 135                 140

tac tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt gga ggc ggt   480
Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
145                 150                 155                 160

tca ggc gga ggt ggc tct ggc ggt ggc gga tcg gac atc gag ctc act   528
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr
                165                 170                 175

cag tct cca ctc tcc ctg cct gtc agt ctt gga gat cag gcc tcc atc   576
Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile
            180                 185                 190

tct tgc aga tct agt cag aac ctt gta cac agt aat gga aat acc tat   624
Ser Cys Arg Ser Ser Gln Asn Leu Val His Ser Asn Gly Asn Thr Tyr
        195                 200                 205

tta cat tgg tac ctg cag aag cca ggc cag tct cca aat ctc ctg atc   672
Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Asn Leu Leu Ile
    210                 215                 220

tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc   720
Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly
225                 230                 235                 240

agt gga tca ggg aca gaa ttc aca ctc aag atc agc aga gtg gag gct   768
Ser Gly Ser Gly Thr Glu Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
                245                 250                 255

gag gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg ctc   816
Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Leu
            260                 265                 270

acg ttc ggt gct ggg acc aag gtg gag ctg aaa cgg gcg gcc gca ggt   864
Thr Phe Gly Ala Gly Thr Lys Val Glu Leu Lys Arg Ala Ala Ala Gly
        275                 280                 285

gcg ccg gtg ccg tat ccg gat ccg ctg gaa ccg cgt gcc gca aag aag   912
Ala Pro Val Pro Tyr Pro Asp Pro Leu Glu Pro Arg Ala Ala Lys Lys
    290                 295                 300

aag tag                                                          918
Lys
305
```

<210> 43
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Amino acid sequence of heavy chain CDR-1

<400> 43
Ser His Gly Val His
1 5

<210> 44
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Amino acid sequence of heavy chain CDR-2

<400> 44
Val Ile Trp Gly Ala Gly Arg Thr Asp Tyr Asn Ala Ala Phe Ile Ser
1 5 10 15

<210> 45
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Amino acid sequence of heavy chain CDR-3

<400> 45
Asn Arg Tyr Glu Ser Tyr Phe Asp Tyr
1 5

<210> 46
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Amino acid sequence of light chain CDR-1

<400> 46
Arg Ser Ser Gln Asn Leu Val His Ser Asn Gly Asn Thr Tyr Leu His
1 5 10 15

<210> 47
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Amino acid sequence of light chain CDR-2

<400> 47
Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe
1 5 10

<210> 48
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Amino acid sequence of light chain CDR-3

<400> 48
Ser Gln Ser Thr His Val Pro Leu Thr
1 5

<210> 49
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 49
gtcccaggat cctctgaagc agtcaggccc 30

<210> 50
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 50
acagtgggcc cgtcgttttg gctgaggaga 30

<210> 51
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 51
tgtgccctcg aggtgactca aactccactc tc 32

<210> 52
<211> 28
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 52
atggatacta gtggtgcagc atcagccc 28

<210> 53
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 53
ctcttggagg agggtgccag 20

<210> 54
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 54
ccagatttca actgctcatc aga 23

<210> 55
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 55
gcggcccagc cggccatggc ccaggtgcag ctgaagcagt cag 43

<210> 56
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 56
agacggtgac cgtggtgcct tggcccc 27

<210> 57
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 57
tcgagctcac tcagtctcca ctctccctgc ct 32

<210> 58
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 58
cacctgcggc cgcccgtttc agctc 25

<210> 59
<211> 305
<212> PRT
<213> Mus sp.

<400> 59

```
Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
  1               5                  10                  15

Ala Gln Pro Ala Met Ala Asp Ile Val Leu Thr Gln Ser Pro Ala Ser
             20                  25                  30

Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser
         35                  40                  45

Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln
     50                  55                  60

Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu
 65                  70                  75                  80

Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
                 85                  90                  95

Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr
            100                 105                 110

Tyr Cys Gln Gln Ser Ser Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr
        115                 120                 125

Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    130                 135                 140
```

```
Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val
145                 150                 155                 160

Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr
                165                 170                 175

Phe Thr Asp Tyr Val Ile Asn Trp Leu Asn Gln Arg Thr Gly Gln Gly
            180                 185                 190

Leu Glu Trp Ile Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ala Tyr Tyr
        195                 200                 205

Asn Glu Met Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser
    210                 215                 220

Asn Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala
225                 230                 235                 240

Val Tyr Phe Cys Ala Arg Arg Gly Thr Gly Thr Gly Phe Ala Tyr Trp
                245                 250                 255

Gly Arg Gly Thr Leu Val Thr Val Ser Ala Ala Ala Ala Ala Asp Tyr Lys
            260                 265                 270

Asp Asp Asp Asp Lys Gly Ser Ser Glu Gln Lys Leu Ile Ser Glu Glu
        275                 280                 285

Asp Leu Gly Ser Arg Ser Thr His His His His His His Gly Ser Thr
    290                 295                 300

Lys
305
```

<210> 60
<211> 305
<212> PRT
<213> Mus sp.

<400> 60

```
Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
  1               5                  10                  15

Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Gln Ser Gly Pro Glu
             20                  25                  30

Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
         35                  40                  45

Tyr Thr Phe Thr Asp Tyr Val Ile Asn Trp Leu Asn Gln Arg Thr Gly
     50                  55                  60

Gln Gly Leu Glu Trp Ile Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ala
 65                  70                  75                  80

Tyr Tyr Asn Glu Met Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys
                 85                  90                  95
```

```
Ser Ser Asn Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
            100                 105                 110

Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Thr Gly Thr Gly Phe Ala
        115                 120                 125

Tyr Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu Thr
145                 150                 155                 160

Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
                165                 170                 175

Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met
            180                 185                 190

Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
        195                 200                 205

Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
    210                 215                 220

Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu
225                 230                 235                 240

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Ser Glu Asp Pro Pro Thr
                245                 250                 255

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ala Ala Ala Asp Tyr Lys
            260                 265                 270

Asp Asp Asp Asp Lys Gly Ser Ser Glu Gln Lys Leu Ile Ser Glu Glu
        275                 280                 285

Asp Leu Gly Ser Arg Ser Thr His His His His His His Gly Ser Thr
    290                 295                 300

Lys
305
```

<210> 61
<211> 118
<212> PRT
<213> Mus sp.

<400> 61

```
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
  1               5                  10                  15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
             20                  25                  30

Val Ile Asn Trp Leu Asn Gln Arg Thr Gly Gln Gly Leu Glu Trp Ile
         35                  40                  45
```

```
Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ala Tyr Tyr Asn Glu Met Phe
    50                  55                  60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Asn Thr Ala Tyr
65                  70                  75                  80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85                  90                  95

Ala Arg Arg Gly Thr Gly Thr Gly Phe Ala Tyr Trp Gly Arg Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ala
        115


<210> 62
<211> 111
<212> PRT
<213> Mus sp.

<400> 62
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
            20                  25                  30

Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45

Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala
    50                  55                  60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65                  70                  75                  80

Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Ser
                85                  90                  95

Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110


<210> 63
<211> 117
<212> PRT
<213> Mus sp.

<400> 63
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1               5                   10                  15

Ser Leu Ser Phe Ile Cys Thr Val Ser Gly Phe Ser Leu Thr Ser His
            20                  25                  30

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
```

```
Gly Val Ile Trp Gly Ala Gly Arg Thr Asp Tyr Asn Ala Ala Phe Ile
     50                  55                  60

Ser Arg Leu Ser Ile Ser Arg Asp Ile Ser Lys Ser Gln Val Phe Phe
 65                  70                  75                  80

Lys Met Asn Ser Leu Gln Val Asp Asp Thr Ala Ile Tyr Tyr Cys Ala
                 85                  90                  95

Arg Asn Arg Tyr Glu Ser Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
            100                 105                 110

Ser Leu Thr Val Ser
        115
```

<210> 64
<211> 113
<212> PRT
<213> Mus sp.

<400> 64

```
Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
  1               5                  10                  15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Leu Val His Ser
            20                  25                  30

Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35                  40                  45

Pro Asn Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
     50                  55                  60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Lys Ile
 65                  70                  75                  80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
                 85                  90                  95

Thr His Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Val Glu Leu Lys
            100                 105                 110

Arg
```

<210> 65
<211> 302
<212> PRT
<213> Mus sp.

<400> 65

```
Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile Phe
  1               5                  10                  15

Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr
            20                  25                  30
```

```
Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu Gln Gln Ser Gly Pro
          35                  40                  45

Gly Leu Val Gln Pro Ser Gln Ser Leu Ser Phe Ile Cys Thr Val Ser
      50                  55                  60

Gly Phe Ser Leu Thr Ser His Gly Val His Trp Val Arg Gln Ser Pro
 65                  70                  75                  80

Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ala Gly Arg Thr
                 85                  90                  95

Asp Tyr Asn Ala Ala Phe Ile Ser Arg Leu Ser Ile Ser Arg Asp Ile
            100                 105                 110

Ser Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Val Asp Asp
        115                 120                 125

Thr Ala Ile Tyr Tyr Cys Ala Arg Asn Arg Tyr Glu Ser Tyr Phe Asp
    130                 135                 140

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
145                 150                 155                 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr
                165                 170                 175

Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile
            180                 185                 190

Ser Cys Arg Ser Ser Gln Asn Leu Val His Ser Asn Gly Asn Thr Tyr
        195                 200                 205

Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Asn Leu Leu Ile
    210                 215                 220

Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly
225                 230                 235                 240

Ser Gly Ser Gly Thr Glu Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
                245                 250                 255

Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Leu
            260                 265                 270

Thr Phe Gly Ala Gly Thr Lys Val Glu Leu Lys Arg Ala Ala Ala Gly
        275                 280                 285

Ala Pro Val Pro Tyr Pro Asp Pro Leu Glu Pro Arg Ala Ala
    290                 295                 300
```

<210> 66
<211> 305
<212> PRT
<213> Mus sp.

<400> 66

```
Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile Phe
  1               5                  10                  15

Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr
             20                  25                  30

Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu Gln Gln Ser Gly Pro
         35                  40                  45

Gly Leu Val Gln Pro Ser Gln Ser Leu Ser Phe Ile Cys Thr Val Ser
     50                  55                  60

Gly Phe Ser Leu Thr Ser His Gly Val His Trp Val Arg Gln Ser Pro
 65                  70                  75                  80

Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ala Gly Arg Thr
                 85                  90                  95

Asp Tyr Asn Ala Ala Phe Ile Ser Arg Leu Ser Ile Ser Arg Asp Ile
            100                 105                 110

Ser Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Val Asp Asp
        115                 120                 125

Thr Ala Ile Tyr Tyr Cys Ala Arg Asn Arg Tyr Glu Ser Tyr Phe Asp
    130                 135                 140

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
145                 150                 155                 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr
                165                 170                 175

Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile
            180                 185                 190

Ser Cys Arg Ser Ser Gln Asn Leu Val His Ser Asn Gly Asn Thr Tyr
        195                 200                 205

Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Asn Leu Leu Ile
    210                 215                 220

Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly
225                 230                 235                 240

Ser Gly Ser Gly Thr Glu Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
                245                 250                 255

Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Leu
            260                 265                 270

Thr Phe Gly Ala Gly Thr Lys Val Glu Leu Lys Arg Ala Ala Ala Gly
        275                 280                 285

Ala Pro Val Pro Tyr Pro Asp Pro Leu Glu Pro Arg Ala Ala Lys Lys
    290                 295                 300
```

Lys
305